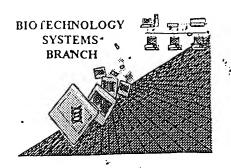
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: $\frac{89/8926/3}{0 \text{ LPE}}$ Source: $\frac{0 \text{ LPE}}{11/26/200/}$

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

PAGE: 1

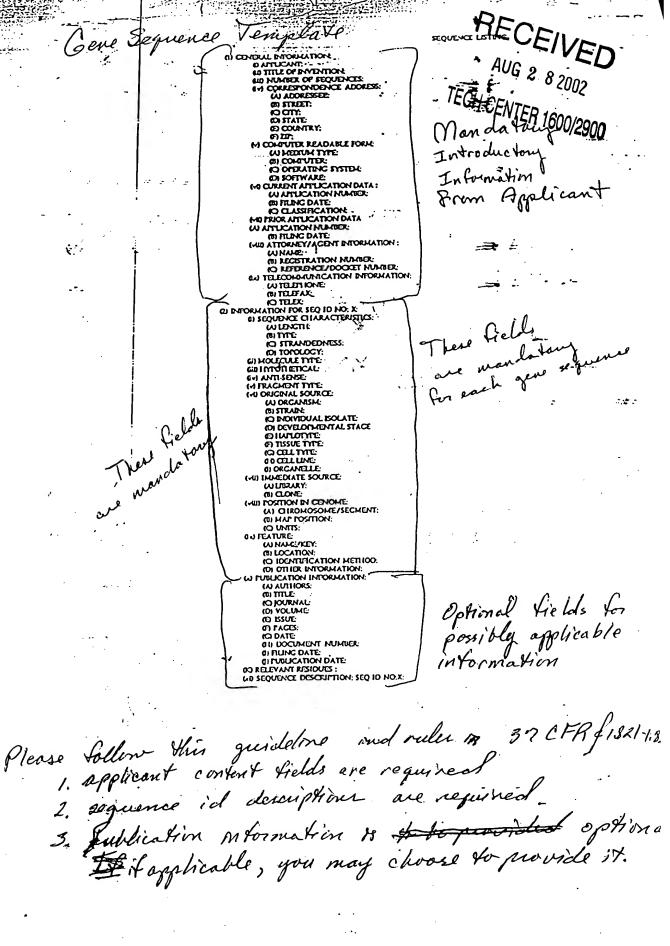
RAW SEQUENCE LISTING PATENT APPLICATION US/09/892,613

DATE: 11/26/2001 TIME: 02:32:09

INPUT SET: S36677.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

1	SEQUENCE LISTING
ERRORE	Applicant name Title of invention Number of sequences See Attached Template See Not Comply Mailing Address is required Corrected Diskette Needed
5 6 7 7 8 8 9 10 110 111 112 110 111 112	(2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY:linear (ii) MOLECULE TYPE: DNA (oligonucleotide) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
20 13 14 20 15 16 17> 18	FR-patched RFB4 Long B Type Nucleic acres WH: Full length CDNA sequence (SEQ ID no. 1):
70 20 21 22 23 24	CTCCTTCAGTATCTATGACATGTCTTGGGTTCGCCAGGCACCGGGAAAGGGGCTGGAGTGGGTCGCATACATTAGTAGTG GTGGTGGTACCACCTACTATCCAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCCCTGTAC CTGCAAATGAACAGTCTGAGGGTGGAGGACACAGCCTTATATTACTGTGCAAGACATAGTGGCTACGGTAGTAGCTACGG GGTTTTGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTTCA
25 26 27 28 > 29 30	EVQLLESGGGLVQPGGSLRLSCAASGFSFSIYDMSWVRQAPGKGLEWVAYISSGGGTTYYPDTVKGRFTISRDNAKNSLY LQMNSLRVEDTALYYCARHSGYGSSYGVLFAYWGQGTLVTVSS
31 32 > 33(34 35 > 36	ACCGGAAAGGGCTGGAGTGGCTCGCATAC 5'Primer for N-template (SEQ ID no. 4) GAGTGCAGCTGCTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCTGAGG 3' Primer for N-template (SEQ ID no. 5)
37 38 39	5 See Attached template for required Fields. 6 Rifer to Federal Register Val 55No 84 Tuesday, May 1,1990
	CFR in 37 CFR Part 1 & 1.821 - § 1.825 for specific guidelines and requirements.



RAW SEQUENCE LISTING PATENT APPLICATION US/09/892,613

DATE: 11/26/2001 TIME: 02:32:10

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```
C-terminal sense strand template DNA sequence (SEQ ID no. 6):
40
         TTCACCATCTCCAGAGACAATGCCAAGAACTCCCTGTACCTGCAAATGAACAGTCTGAGGGTGGAGGACACAGCCTTATA
41
         5' Primer for C-template (SEQ ID no. 7)
         GGTGGTACCACCTACTATCCAGACACTGTGAAGGGCCGATTCACCATCTCCAGAGACAAT
         3' Primer for C-template (SEQ ID no. 8)
         tippe moleic aviel c DNA ete.
49
         Joining site: KpnI
50
                                                                                             se template
51
52
53
         Full length cDNA sequence (SEQ ID no. 9)
54
         GATATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCCTCTGTGGGAGACAGAGTCACCATTAGTTGCAGGGCAAGTCA
55
         GGACATTAGCAATTATTTAAACTGGTATCAGCAGAAACCAGGTAAGGCTCCGAAACTCCTGATCTACTACACTAGTATAT
56
         TACACTCAGGAGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGAACAGAATTTACTCTCACCATTAGCTCCCTGCAGCCA
57
         GAAGATTTTGGCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGAGGCACCAAGGTGGAAATCAA

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58
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60
         Full length amino acid sequence (SEQ ID no.
61
         DIQMTQSPSSLSASVGDRVTISCRASQDISNYLNWYQQKPGKAPKLLIYYTSILHSGVPSRFSGSGSCTEFTLTISSLQP
62
         EDFATYFCQQGNTLPWTFGGGTKVEIK
63
                                                          1. sequence characteristics
64
        N-terminal sense strand template DNA sequence (SEQ ID no. 11)
65
         CTGTCTGCCTCTGTGGGAGACAGAGTCACCATTAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTAAACTGGTATCA
66
         GCAGAAACCAGGTAAGGCTCCGAAACTC
67
                                                                sequence characters tres
68
                                                                                                                 Format Fields Begin
      (5' Primer for N template )(SEQ ID no. 12)
69
         GATATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTGGGAGAC
70
71
         3' Primer for N-template (SEQ ID no. 13)
72
         ATATACTAGTGTAGTAGATCAGGAGTTTCGGAGCCTTACC
73
        C-terminal sense strand template DNA sequence (SEQ ID no. 14)
74
75
        CCATCAAGGTTCAGTGGCAGTGGGTCTGGAACAGAATTTACTCTCACCATTAGCTCCCTGCAGCCAGAAGATTTTGCCAC
76
77
         TTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTC
78
       (5' Primer for C-template (SEQ ID no. 15)
79
         CTACACTAGTATATTACACTCAGGAGTCCCATCAAGGTTCAGTGGCAGT
80
81
         3' Primer for C-template (SEQ ID no. 16)
82
         TTTGATTTCCACCTTGGTGCCTCCACCGAACGTCCACGGAAGCGTATT
83
                                                                                  Each requence must be identified according to the rules, template and enclosed example corrections
84
         Joining site: SpeI A(CTAG(T
85
86
87
88
        FR-Patched chimeric 1F5
89
90
        VH:
91
        Full length cDNA sequence (SEQ ID no. 17):
```

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/892,613

DATE: 11/26/2001 TIME: 02:32:10

INPUT SET: S36677.raw

CAGGTGCAACTGGTGGCTTCCGGGGCTGAGGTAAATAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTA 93 94 CACATTTACCAGTTACAATATGCACTGGGTACGGCAGCCTCCTGGAAGGGGCCTGGAATGGATTGGAGCTATTTATCCAG GAAATGGTGATACTAGTTACAATCAGAAATTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 95 ATGCAGCTCAGCAGTCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGCACTACGGTAGTAACTACGTAGA 96 CTACTTTGACTACTGGGGCCAAGGCACCACTGTTACAGTCTCCTCTGATCA 97

98

- 99 Full-length amino acid sequence (SEQ ID no. 18):
 - QVQLVASGAEVNKPGASVKVSCKASGYTFTSYNMHWVRQPPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAY 100

MQLSSLTSEDSAVYYCARSHYGSNYVDYFDYWGQGTTVTVSSD 101

102 103

- 21. Sequence charactustics. mulecule type

 N-terminal sense strand template DNA sequence (SEQ ID no. 19): 104
 - AATAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTACG 105 106 GCAGCCTCCTGGAAGGGGCCTGGAATGGATTGGA

107 108

- 5' Primer for N-template (SEQ ID no. 20)
- 109 CAGGTGCAACTGGTGGCTTCCGGGGCTGAGGTAAATAAGCCTGGGGCCTCAGTGAAG

110

- 111 3' Primer for N-template (SEQ ID no. 21)
 - TGTAACTAGTATCACCATTTCCTGGATAAATAGCTCCAATCCATTCCAGGCCCCT 112

113

- C-terminal sense strand template DNA sequence (SEQ ID no. 22): 114
 - 115 TTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGTCTGACATCTGAGGACTCTGCGGTCTATTACTG

116 TGCAAGATCGCACTACGGTAGTAACTACGTAGACTACTTTGACTAC

117

- 118 5' Primer for C-template (SEQ ID no. 23)
- 119 TGATACTAGTTACAATCAGAAATTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCC

120

- 121 3' Primer for C-template (SEQ ID no. 24)
- TGATCAGAGGAGACTGTAACAGTGGTGCCTTGGCCCCAGTAGTCAAAGTAGTCTACGTA 122

123

Joining site: SpeI 124

125

127

128

126

in Male coulety gre Full-Tength/cDNA sequence (SEQ ID no. 25):

- 129 GAYATTCAACTCACACAGTCTCCATCAAGTCTTTCTGCATCTGTGGGGGACAGAGTCACAATTACTTGCAGGGCCAGCTC
- 130 AAGTTTAAGTTTCATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCACATCCAACCTGG
- $\tt CTTCCGGAGTCCCTAGTCGCTTCAGTGGCAGTGGGTCTGGGACCGAGTTCACTCTCACAATCAGCAGTTTGCAGCCTGAA$ 131
- 132 GATTTCGCCACTTATTTCTGCCATCAGTGGAGTAGTAACCCGCTCACGTTCGGTGCTGGGACCAAGCTGACCGTTCTACG

133

134 135

- Full-length amino acid sequence (SEQ ID no. 26):
- 136 DIQLTQSPSSLSASVGDRVTITCRASSSLSFMHWYQQKPGSSPKPWIYATSNLASGVPSRFSGSGSGTEFTLTISSLQPE 137 DFATYFCHQWSSNPLTFGAGTKLTVLR

138

- 139 N-terminal sense strand template DNA sequence (SEO ID no. 27):
 - TCAAGTCTTTCTGCATCTGTGGGGGACAGAGTCACAATTACTTGCAGGGCCAGCTCAAGTTTAAGTTTCATGCACTGGTA 140 141 CCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCACATCC

142

- 143 5' Primer for N-template (SEQ ID no. 28):
 - GATATTCAACTCACACAGTCTCCATCAAGTCTTTCTGCATCTGTG 144

145

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/892,613

DATE: 11/26/2001 TIME: 02:32:11

INPUT SET: S36677.raw

		INFUI SEI: 3500/7.74W
>	146	3' Primer for N-template (SEQ ID no. 29):
	147	GGACTCCGGAAGCCAGGTTGGATGTGGCATAAATCCAGGG
	148	
>	149	C-terminal sense strand template DNA sequence (SEQ ID no. 30):
	150	${\tt TTCAGTGGCAGTGGGTCTGGGACCGAGTTCACTCTCACAATCAGCAGTTTGCAGCCTGAAGATTTCGCCACTTATTTCTG}$
	151	CCATCAGTGGAGTAGTAACCCGCTCACGTTCGGTGCTGGG
	152	
>	153	5' Primer for C-template (SEQ ID no. 31):
	154	GGCTTCCGGAGTCCCTAGTCGCTTCAGTGGCAGTGGGTCTGGG
	155	
>	156	3' Primer for C-template (SEQ ID no. 32):
	157	CCGTAGAACGGTCAGCTTGGTCCCAGCACCGAACGTGAGCGG
	158	
	159	Joining site: BspEI
	160	
	161	

1. Lines 5-12 are the beginning of an extended format required for sequence latings.

2. Refer to the rules of 37 CFR Part 1 Rules of Practice on Patent Cases according to \$1.82) - \$1.825

(Set foth on The Federal Register Vol 55, No 84

Tuesday, May 1,1990 — Rules and Regulations

3. Use The Template attached and the CFR rules are a guide

4. Call Mark Spencer at the Help Dask

for additional assistance 70 3 30 8 4212